

22. (Amended) A method of modifying, by computer, the expression of different gene collections in a genome, comprising detecting changes in expression of different gene collections in a genome that result in changes in the level of connectron control sequences caused by an exogenous stimulus.

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23. (Amended) A method of detecting, by computer, where and when new genes have been integrated into a host genome comprising detecting an operable link between a newly introduced gene and a preexisting connectron behavior in said host genome.

24. (Amended) A method of detecting, by computer, the expression effect of different gene collections in a given host genome, comprising detecting the effect of connectrons on transcription.

25. (Amended) A method of changing the expression of different gene collections in a genome comprising modifying, by a computer, mediated method identification of connectron organization.

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28. (Amended) Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequence and the RNA molecule can form a the tetradic relationship such that  $T1=C1$  and  $T2=C2$  where  $T1$  and  $T2$  are DNA sequences 20 or more bases in length, where the  $C1$  sequence is adjacent to the  $C2$  sequence, where the  $T1$  and  $T2$  sequences are on the same chromosome, and where the  $C1/C2$  sequences are on the same chromosome as  $T1$  and  $T2$  or where the  $C1/C2$  sequences are on a chromosome different from  $T1$  and  $T2$ , wherein:

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10 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the  $C2$  sequence must occur in the same chromosome as the  $C1$  sequence,

15 C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

20 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

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25 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

5 29. (Amended) Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits many different C1/C2 short loops to control the existence of a T1-T2 long loop and wherein said C1/C2 short lops can be on the same chromosome or on different chromosomes from the T1-T2 long loop, wherein:

10 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 540 or more bases such that the C1 sequence is adjacent to the C2 sequence,

20 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

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T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

5 30. (Amended) Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits one C1/C2 short loop to control the existence of many T1-T2 long loops, the C1/C2 short loop can be on the same chromosome or on different chromosomes from the T1-T2 long loops, wherein:

10 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

20 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

25 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

31. (Amended) Using the method as defined in claim 20, where the DNA sequences and the RNA molecule function as a connectron between prokaryotes and their plasmids and wherein said connectron implements a control mechanism between the two genomes that makes  
5 it possible from them to form a symbiotic relationship, and in the case of D. radiodurans the relationship is not symmetric, and the D. radiodurans genome sends C1/C2 short loops to the MP1 plasmid, wherein:

10 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 40 or  
more bases such that the C1 sequence is adjacent to the C2  
sequence,

20 T1 sequence - any positive or negative strand DNA sequence of  
20 bases or more that is on the same chromosome as the T2  
sequence, the T1 and T2 sequences must be between about 1kb  
and 105kb apart, and

25 T2 sequence - any positive or negative strand DNA sequence of  
20 bases or more that is on the same chromosome as the T1  
sequence, the T2 or T1 sequences must be between about 1kb and  
105kb apart.

32. (Amended) Using the method as defined in claim 20, where the  
DNA sequences and the RNA molecule function as a connectron that  
exist in a plant or a higher animal.

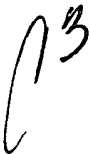
33. (Amended) Using the method as defined in claim 20, in  
prokaryotes, archaea, single-celled eukaryotes and multi-celled  
eukaryotes, where the DNA sequences and the RNA molecule function  
as a connectron that permits one C1/C2 short loop to control the  
5 existence of one or more T1-T2 long loops without being subject to  
any expression controls other than those of the gene to which the  
C1/C2 is 3'UTR, wherein:

10 C1 sequence - any positive or negative strand DNA sequence of  
20 bases or more, the C2 sequence must occur in the same  
chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of  
20 bases or more, the C1 sequence must occur in the same  
chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

20 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart,

25  T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart, and

3'UTR - untranslated 3' end of an mRNA is beyond the end of the last exon, a stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

5 34. (Amended) Using the method as defined in claim 20, in prokaryotes, archea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits one C1/C2 short loop to control the existence of one or more T1-T2 long loops such that this C1/C2 short loop is itself subject to expression control by another T1-T2 long loop which surrounds it, wherein:

10 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

15 C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

20 C3 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

35. (Amended) Using the method as defined in claim 20, in prokaryotes, archaea, single-celled eukaryotes and multi-celled eukaryotes, where the DNA sequences and the RNA molecule function as a connectron that permits one C1/C2 short loop to control the  
5 existence of the T1-T2 long loop that surrounds it, wherein:

C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

10 C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

C1/C2 - any positive or negative strand DNA sequence of 50 or more bases such that the C1 sequence is adjacent to the C2 sequence,

15 T1 sequence - any positive or negative strand DNA sequence of 20bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

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T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

36. (Amended) Using the method as defined in claim 20, where the DNA sequences and the RNA molecule function as a connectron that do not have any genes within the T1-T2 long loop, wherein:

5 T1 sequence is any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, and

10 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, and the T2 or T1 sequences must be between about 1kb and 105kb apart.

37. (Amended) Using the method as defined in claim 20, where the DNA sequences and the RNA molecule function as a geneless connectron where one C1/C2 short loop controls the existence of many geneless T1-T2 long loops, wherein:



5 C1 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C2 sequence must occur in the same chromosome as the C1 sequence,

10 C2 sequence - any positive or negative strand DNA sequence of 20 bases or more, the C1 sequence must occur in the same chromosome as the C2 sequence,

13 C1/C2 - any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence,

15 T1 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T2 sequence, the T1 and T2 sequences must be between about 1kb and 105kb apart, and

20 T2 sequence - any positive or negative strand DNA sequence of 20 bases or more that is on the same chromosome as the T1 sequence, the T2 or T1 sequences must be between about 1kb and 105kb apart.

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